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SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> Plasmid vectors for transformation of filamentous fungi

<130> Polyketide Synthetase

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<170> PatentIn Ver. 2.1

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Arg Phe Ala Pro Pro Leu Lys Asp Leu Leu Leu Lys Gly Asn Ser Pro
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tac ttg aca cat ttt gtt aaa caa gtt cac gca ctt ctt aga agg gag 144
Tyr Leu Thr His Phe Val Lys Gln Val His Ala Leu Leu Arg Arg Glu
      35              40              45

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Ile Ser Ser Leu Pro Ala Val Gln Gln Lys Leu Phe Pro Asn Phe Ala
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His Phe Tyr Asp Gly Gln Gly Arg Thr Phe Pro Ser Glu Asn Ser Arg
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Ile Ile Gly Leu Cys Val Gly Ser Leu Ala Ala Thr Ala Val Ser Cys
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11

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Val	Ala	Leu	His	Val	Gly	Leu	Arg	Val	Trp	Arg	Thr	Thr	Ser	Leu	Phe	
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Ile	Glu	Met	Gly	Leu	Ala	Arg	Ser	Ser	Val	Pro	Tyr	Ile	Ser	Ser	Val	
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Ala	His	His	Asn	Met	Thr	Ile	Ser	Gly	Pro	Pro	Ser	Val	Leu	Glu	Lys	
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Ile	Tyr	Ala	Pro	Tyr	His	Ala	Ser	His	Leu	Tyr	Ser	Met	Asp	Asp	Val	
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Tyr	Ala	Asp	Leu	Leu	Arg	Cys	Cys	Val	Ser	Asp	Met	Leu	Ile	Gln	Pro	
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Leu	Asp	Leu	Thr	Lys	Val	Ser	Gln	Ala	Val	Ala	Gln	Leu	Leu	Glu	Val	
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Asn	Ser	Leu	Val	Ser	Val	Leu	Glu	Pro	Thr	Leu	Ala	Glu	Arg	Cys	Ala	
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12

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Cys	Asn	Ser	Leu	Trp	Arg	Asn	Asp	Cys	Asp	Thr	Ala	Ile	Ala	Gly	Gly	
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13

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Asp Gly Tyr Cys Arg Ala Asp Gly Val Gly Thr Ile Ile Leu Lys Arg	
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Gly Ala Tyr Thr Asn His Ser Ala Glu Ala Val Ser Ile Thr Arg Pro	
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Lys Ser Phe Gly Val Glu Pro Gly Phe Val Leu Gly His Ser Leu Gly	
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His Tyr Ala Ala Leu His Val Ala Gly Val Leu Ser Ala Asn Asp Thr	
1010 1015 1020	

15

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16

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17

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Pro Ser Arg Met Asp Val Pro Pro Val Arg Ser Gly Glu Gly Pro Pro	
1635 1640 1645	
act tca gca ccc acg cag caa gct atc gct ctg ccg ttc gca gcc gat	4992
Thr Ser Ala Pro Thr Gln Gln Ala Ile Ala Leu Pro Phe Ala Ala Asp	
1650 1655 1660	
aca tcc atg gac tcc cga ttg aga cct ctt ctt cgc atc ttg tca gaa	5040
Thr Ser Met Asp Ser Arg Leu Arg Pro Leu Leu Arg Ile Leu Ser Glu	
1665 1670 1675 1680	
gag atc ggt ctc ggt ctt gac gtt ctt tcg gac gat gaa ctc gac ttt	5088
Glu Ile Gly Leu Gly Leu Asp Val Leu Ser Asp Asp Glu Leu Asp Phe	
1685 1690 1695	

18

gcg gac cac ggt gtc gac tca ctc ctc tca ttg acc atc act ggt cgc	5136
Ala Asp His Gly Val Asp Ser Leu Leu Ser Leu Thr Ile Thr Gly Arg	
1700 1705 1710	
atg cgt gag gaa ttg ggt ctc gac gtt gaa tct aca gca ttc atg aac	5184
Met Arg Glu Glu Leu Gly Leu Asp Val Glu Ser Thr Ala Phe Met Asn	
1715 1720 1725	
tgt ccc act ttg ggc agc ttt aaa ttg ttc cta gga ctt gtc gat cag	5232
Cys Pro Thr Leu Gly Ser Phe Lys Leu Phe Leu Gly Leu Val Asp Gln	
1730 1735 1740	
gac aat aag ggc agc agc ggc agt gat ggc agt ggt agg agc agt cca	5280
Asp Asn Lys Gly Ser Ser Gly Ser Asp Gly Ser Gly Arg Ser Ser Pro	
1745 1750 1755 1760	
gca ccg ggt acc gag tct ggc gct act aca cca cct atg agc gaa gag	5328
Ala Pro Gly Thr Glu Ser Gly Ala Thr Thr Pro Pro Met Ser Glu Glu	
1765 1770 1775	
gac cag gac aag ata gtc agc agt cac tcg ctt cac cag ttc caa gcc	5376
Asp Gln Asp Lys Ile Val Ser Ser His Ser Leu His Gln Phe Gln Ala	
1780 1785 1790	
agt tcg acg ctt cta cag ggc agt ccc agt aaa gct cgc tcg act ttg	5424
Ser Ser Thr Leu Leu Gln Gly Ser Pro Ser Lys Ala Arg Ser Thr Leu	
1795 1800 1805	
ttc ttg cta cca gat ggc tcg gga tct gcc aca tcc tac gct tcc ctt	5472
Phe Leu Leu Pro Asp Gly Ser Gly Ser Ala Thr Ser Tyr Ala Ser Leu	
1810 1815 1820	
ccc ccg atc tct cca gac gga gat gtt gct gtc tac ggg ttg aac tgt	5520
Pro Pro Ile Ser Pro Asp Gly Asp Val Ala Val Tyr Gly Leu Asn Cys	
1825 1830 1835 1840	
cca tgg ctg aag gac tct agt tac ctc gtc gag ttt gga ctc aag ggc	5568
Pro Trp Leu Lys Asp Ser Ser Tyr Leu Val Glu Phe Gly Leu Lys Gly	
1845 1850 1855	
ttg aca gag ctc tat gtc aac gag ata ctc cgt cgc aag cca cag ggt	5616
Leu Thr Glu Leu Tyr Val Asn Glu Ile Leu Arg Arg Lys Pro Gln Gly	
1860 1865 1870	
cct tac aat ttg gga gga tgg tca gcc ggt ggc att tgc gct tat gaa	5664
Pro Tyr Asn Leu Gly Gly Trp Ser Ala Gly Gly Ile Cys Ala Tyr Glu	
1875 1880 1885	
gct gcc ctg atc ctc acc aga gca gga cac caa gtc gat cgc ctt atc	5712
Ala Ala Leu Ile Leu Thr Arg Ala Gly His Gln Val Asp Arg Leu Ile	
1890 1895 1900	
ttg att gac tct ccc aat ccc gtt ggt ctt gag aag cta cct cct cgc	5760
Leu Ile Asp Ser Pro Asn Pro Val Gly Leu Glu Lys Leu Pro Pro Arg	
1905 1910 1915 1920	

19

ttg tac gat ttc ctc aat tcg cag aat gtc ttt gga tca gac aac ccg 5808
 Leu Tyr Asp Phe Leu Asn Ser Gln Asn Val Phe Gly Ser Asp Asn Pro
 1925 1930 1935

cac agc act gct gga aca agc gtc aaa gct cca gaa tgg ctt ctt gca 5856
 His Ser Thr Ala Gly Thr Ser Val Lys Ala Pro Glu Trp Leu Leu Ala
 1940 1945 1950

cat ttc ctg gcc ttc att gac gct ctg gat gct tat gtc gca gtg cct 5904
 His Phe Leu Ala Phe Ile Asp Ala Leu Asp Ala Tyr Val Ala Val Pro
 1955 1960 1965

tgg gac tct ggt cta gtc ggt cta gca tca ccg ctc cct gca ccg ccg 5952
 Trp Asp Ser Gly Leu Val Gly Leu Ala Ser Pro Leu Pro Ala Pro Pro
 1970 1975 1980

cag aca tac atg ctg tgg gca gaa gac gga gtt tgc aaa gac tct gat 6000
 Gln Thr Tyr Met Leu Trp Ala Glu Asp Gly Val Cys Lys Asp Ser Asp
 1985 1990 1995 2000

agt gct cgt ccc gag tac cgt gac gat gac cca cgc gag atg aga tgg 6048
 Ser Ala Arg Pro Glu Tyr Arg Asp Asp Asp Pro Arg Glu Met Arg Trp
 2005 2010 2015

ctg ttg gag aac aga aca aac ttt ggt ccg aat ggt tgg gag gcg cta 6096
 Leu Leu Glu Asn Arg Thr Asn Phe Gly Pro Asn Gly Trp Glu Ala Leu
 2020 2025 2030

ctt ggt ggt aaa gag ggt ttg ttc atg gat cgg att gcg gaa gcg aat 6144
 Leu Gly Gly Lys Glu Gly Leu Phe Met Asp Arg Ile Ala Glu Ala Asn
 2035 2040 2045

cat ttt agt atg ttg aag aga gga cgg aat gcg gaa tat gtc tct gca 6192
 His Phe Ser Met Leu Lys Arg Gly Arg Asn Ala Glu Tyr Val Ser Ala
 2050 2055 2060

ttc ctg gct cgg gcc ttg gac aat tag 6219
 Phe Leu Ala Arg Ala Leu Asp Asn
 2065 2070

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 <212> PRT
 <213> *Fusarium graminearum*

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 Met Thr Pro Ser Met Met Glu Val Phe Val Phe Gly Asp Gln Ser Thr
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 Arg Phe Ala Pro Pro Leu Lys Asp Leu Leu Leu Lys Gly Asn Ser Pro
 20 25 30
 Tyr Leu Thr His Phe Val Lys Gln Val His Ala Leu Leu Arg Arg Glu
 35 40 45

20

Ile	Ser	Ser	Leu	Pro	Ala	Val	Gln	Gln	Lys	Leu	Phe	Pro	Asn	Phe	Ala	50	55	60	
Asp	Ile	Gln	Glu	Leu	Val	Ser	Lys	Ser	Asp	Trp	Gly	Ser	Gly	Asn	Pro	65	70	75	80
Ala	Leu	Thr	Ser	Ala	Leu	Ala	Cys	Phe	Tyr	His	Leu	Cys	Ser	Phe	Ile	85	90	95	
His	Phe	Tyr	Asp	Gly	Gln	Gly	Arg	Thr	Phe	Pro	Ser	Glu	Asn	Ser	Arg	100	105	110	
Ile	Ile	Gly	Leu	Cys	Val	Gly	Ser	Leu	Ala	Ala	Thr	Ala	Val	Ser	Cys	115	120	125	
Ser	Thr	Ser	Leu	Ser	Glu	Leu	Val	Ser	Ala	Gly	Val	Asp	Ala	Val	Arg	130	135	140	
Val	Ala	Leu	His	Val	Gly	Leu	Arg	Val	Trp	Arg	Thr	Thr	Ser	Leu	Phe	145	150	155	160
Asp	Val	Pro	Asp	Arg	Pro	Ser	Ala	Thr	Trp	Phe	Ile	Ile	Val	Pro	Glu	165	170	175	
Ala	Val	Leu	Pro	Arg	Glu	Ser	Ala	Gln	Asp	Arg	Leu	Asp	Ser	Phe	Ile	180	185	190	
Ile	Glu	Met	Gly	Leu	Ala	Arg	Ser	Ser	Val	Pro	Tyr	Ile	Ser	Ser	Val	195	200	205	
Ala	His	His	Asn	Met	Thr	Ile	Ser	Gly	Pro	Pro	Ser	Val	Leu	Glu	Lys	210	215	220	
Phe	Ile	His	Ser	Ile	Ser	Thr	Ser	Pro	Lys	Asp	Ser	Leu	Pro	Val	Pro	225	230	235	240
Ile	Tyr	Ala	Pro	Tyr	His	Ala	Ser	His	Leu	Tyr	Ser	Met	Asp	Asp	Val	245	250	255	
Asp	Glu	Val	Leu	Ser	Leu	Ser	Ala	Pro	Ser	Phe	Ala	Ser	Glu	Ser	Ile	260	265	270	
Ile	Pro	Leu	Ile	Ser	Ser	Ser	Ser	Gly	Asp	Glu	Leu	Gln	Pro	Leu	Lys	275	280	285	
Tyr	Ala	Asp	Leu	Leu	Arg	Cys	Cys	Val	Ser	Asp	Met	Leu	Ile	Gln	Pro	290	295	300	
Leu	Asp	Leu	Thr	Lys	Val	Ser	Gln	Ala	Val	Ala	Gln	Leu	Leu	Glu	Val	305	310	315	320
Ser	Ser	Ser	Thr	Arg	Ala	Ile	Ile	Lys	Pro	Ile	Ala	Thr	Ser	Val	Ser	325	330	335	
Asn	Ser	Leu	Val	Ser	Val	Leu	Glu	Pro	Thr	Leu	Ala	Glu	Arg	Cys	Ala	340	345	350	

21

Val	Asp	Asn	Ser	Met	Gly	Pro	Lys	Ala	Ser	Thr	Ser	His	Ser	Ser	Ala	355	360	365	
Glu	Thr	Gln	Thr	Glu	Ser	Ser	Ser	Lys	Asn	Ser	Lys	Ile	Ala	Ile	Val	370	375	380	
Ala	Met	Ser	Gly	Arg	Phe	Pro	Asp	Ala	Ala	Asp	Leu	Ser	Glu	Phe	Trp	385	390	395	400
Asp	Leu	Leu	Tyr	Glu	Gly	Arg	Asp	Val	His	Arg	Gln	Ile	Pro	Glu	Asp	405	410	415	
Arg	Phe	Asn	Ala	Glu	Leu	His	Tyr	Asp	Ala	Thr	Gly	Arg	Arg	Lys	Asn	420	425	430	
Thr	Ser	Lys	Val	Met	Asn	Gly	Cys	Phe	Ile	Lys	Glu	Pro	Gly	Leu	Phe	435	440	445	
Asp	Ala	Arg	Phe	Phe	Asn	Met	Ser	Pro	Lys	Glu	Ala	Glu	Gln	Ser	Asp	450	455	460	
Pro	Gly	Gln	Arg	Met	Ala	Leu	Glu	Thr	Ala	Tyr	Glu	Ala	Leu	Glu	Met	465	470	475	480
Ala	Ser	Ile	Val	Pro	Asp	Arg	Thr	Pro	Ser	Thr	Gln	Arg	Asp	Arg	Val	485	490	495	
Gly	Val	Phe	Tyr	Gly	Met	Thr	Ser	Asp	Asp	Trp	Arg	Glu	Val	Asn	Ser	500	505	510	
Gly	Gln	Asn	Val	Asp	Thr	Tyr	Phe	Ile	Pro	Gly	Gly	Asn	Arg	Ala	Phe	515	520	525	
Thr	Pro	Gly	Arg	Leu	Asn	Tyr	Phe	Phe	Lys	Phe	Ser	Gly	Pro	Ser	Ala	530	535	540	
Ser	Val	Asp	Thr	Ala	Cys	Ser	Ser	Ser	Leu	Val	Gly	Leu	His	Leu	Ala	545	550	555	560
Cys	Asn	Ser	Leu	Trp	Arg	Asn	Asp	Cys	Asp	Thr	Ala	Ile	Ala	Gly	Gly	565	570	575	
Thr	Asn	Val	Met	Thr	Asn	Pro	Asp	Asn	Phe	Ala	Gly	Leu	Asp	Arg	Gly	580	585	590	
His	Phe	Leu	Ser	Arg	Thr	Gly	Asn	Cys	Asn	Thr	Phe	Asp	Asp	Gly	Ala	595	600	605	
Asp	Gly	Tyr	Cys	Arg	Ala	Asp	Gly	Val	Gly	Thr	Ile	Ile	Leu	Lys	Arg	610	615	620	
Leu	Glu	Asp	Ala	Glu	Ala	Asp	Asn	Asp	Pro	Ile	Leu	Gly	Val	Ile	Leu	625	630	635	640
Gly	Ala	Tyr	Thr	Asn	His	Ser	Ala	Glu	Ala	Val	Ser	Ile	Thr	Arg	Pro	645	650	655	

22

His	Ala	Gly	Ala	Gln	Glu	Tyr	Ile	Phe	Ser	Lys	Leu	Leu	Arg	Glu	Ser	660	665	670
Gly	Thr	Asp	Pro	Tyr	Asn	Val	Ser	Tyr	Ile	Glu	Met	His	Gly	Thr	Gly	675	680	685
Thr	Gln	Ala	Gly	Asp	Ala	Thr	Glu	Met	Thr	Ser	Val	Leu	Lys	Thr	Phe	690	695	700
Ala	Pro	Thr	Ser	Gly	Phe	Gly	Gly	Arg	Leu	Pro	His	Gln	Asn	Leu	His	705	710	715
Leu	Gly	Ser	Val	Lys	Ala	Asn	Val	Gly	His	Gly	Glu	Ser	Ala	Ser	Gly	725	730	735
Ile	Ile	Ala	Leu	Ile	Lys	Thr	Leu	Leu	Met	Met	Glu	Lys	Asn	Met	Ile	740	745	750
Pro	Pro	His	Cys	Gly	Ile	Lys	Thr	Lys	Ile	Asn	His	His	Phe	Pro	Thr	755	760	765
Asp	Leu	Thr	Gln	Arg	Asn	Val	His	Ile	Ala	Lys	Val	Pro	Thr	Ser	Trp	770	775	780
Thr	Arg	Ser	Gly	Gln	Ala	Asn	Pro	Arg	Ile	Ala	Phe	Val	Asn	Asn	Phe	785	790	795
Ser	Ala	Ala	Gly	Gly	Asn	Ser	Ala	Val	Leu	Leu	Gln	Asp	Ala	Pro	Gln	805	810	815
Pro	Ser	Val	Val	Ser	Asp	Val	Thr	Asp	Pro	Arg	Thr	Ser	His	Val	Val	820	825	830
Thr	Met	Ser	Ala	Arg	Ser	Ala	Asp	Ser	Leu	Arg	Lys	Asn	Leu	Ala	Asn	835	840	845
Leu	Lys	Glu	Leu	Val	Glu	Gly	Gln	Gly	Asp	Ser	Glu	Val	Gly	Phe	Leu	850	855	860
Ser	Lys	Leu	Ser	Tyr	Thr	Thr	Thr	Ala	Arg	Arg	Met	His	His	Gln	Phe	865	870	875
Arg	Ala	Ser	Val	Thr	Ala	Gln	Thr	Arg	Glu	Gln	Leu	Leu	Lys	Gly	Leu	885	890	895
Asp	Ser	Ala	Ile	Glu	Arg	Gln	Asp	Val	Lys	Arg	Ile	Pro	Ala	Ala	Ala	900	905	910
Pro	Ser	Val	Gly	Phe	Val	Phe	Ser	Gly	Gln	Gly	Ala	Gln	Tyr	Arg	Gly	915	920	925
Met	Gly	Lys	Glu	Tyr	Phe	Thr	Ser	Phe	Thr	Ala	Phe	Arg	Ser	Glu	Ile	930	935	940
Met	Ser	Tyr	Asp	Ser	Ile	Ala	Gln	Ala	Gln	Gly	Phe	Pro	Ser	Ile	Leu	945	950	955

23

Pro Leu Ile Arg Gly Glu Val Glu Ala Asp Ser Leu Ser Pro Val Glu
 965 970 975

Ile Gln Leu Gly Leu Thr Cys Leu Gln Met Ala Leu Ala Lys Leu Trp
 980 985 990

Lys Ser Phe Gly Val Glu Pro Gly Phe Val Leu Gly His Ser Leu Gly
 995 1000 1005

His Tyr Ala Ala Leu His Val Ala Gly Val Leu Ser Ala Asn Asp Thr
 1010 1015 1020

Ile Tyr Leu Thr Gly Ile Arg Ala Gln Leu Leu Val Asp Lys Cys Gln
 1025 1030 1035 1040

Ala Gly Thr His Ser Met Leu Ala Val Arg Ala Ser Leu Leu Gln Ile
 1045 1050 1055

Gln Gln Phe Leu Asp Ala Asn Ile His Glu Val Ala Cys Val Asn Gly
 1060 1065 1070

Ser Arg Glu Val Val Ile Ser Gly Arg Val Ala Asp Ile Asp Gln Leu
 1075 1080 1085

Val Gly Leu Leu Ser Ala Asp Asn Ile Lys Ala Thr Arg Val Lys Val
 1090 1095 1100

Pro Phe Ala Phe His Ser Ala Gln Val Asp Pro Ile Leu Ser Asp Leu
 1105 1110 1115 1120

Asp Thr Ala Ala Ser Arg Val Thr Phe His Ser Leu Gln Ile Pro Val
 1125 1130 1135

Leu Cys Ala Leu Asp Ser Ser Val Ile Ser Pro Gly Asn His Gly Val
 1140 1145 1150

Ile Gly Pro Leu His Leu Gln Arg His Cys Arg Glu Thr Val Asn Phe
 1155 1160 1165

Glu Gly Ala Leu His Ala Ala Glu His Glu Lys Ile Ile Asn Lys Thr
 1170 1175 1180

Ser Thr Leu Trp Ile Glu Ile Gly Pro His Val Val Cys Ser Thr Phe
 1185 1190 1195 1200

Leu Lys Ser Ser Leu Gly Pro Ser Thr Pro Ala Ile Ala Ser Leu Arg
 1205 1210 1215

Arg Asn Asp Asp Cys Trp Lys Val Leu Ala Asp Gly Leu Ser Ser Leu
 1220 1225 1230

Tyr Ser Ser Gly Leu Thr Ile Asp Leu Asn Glu Tyr His Arg Asp Phe
 1235 1240 1245

Lys Ala Ser His Gln Val Leu Arg Leu Pro Cys Tyr Ser Trp Glu His
 1250 1255 1260

24

Lys Asn Tyr Trp Ile Gln Tyr Lys Tyr Asp Trp Ser Leu Ala Lys Gly
 265 1270 1275 1280
 Asp Pro Pro Ile Ala Pro Asn Ser Ser Val Glu Ala Val Ser Ala Leu
 1285 1290 1295
 Ser Thr Pro Ser Val Gln Lys Ile Leu Gln Glu Thr Ser Leu Asp Gln
 1300 1305 1310
 Val Leu Thr Ile Val Ala Glu Thr Asp Leu Ala Ser Pro Leu Leu Ser
 1315 1320 1325
 Glu Val Ala Gln Gly His Arg Val Asn Gly Val Lys Val Cys Thr Ser
 1330 1335 1340
 Ser Val Tyr Ala Asp Val Gly Leu Thr Leu Gly Lys Tyr Ile Leu Asp
 345 1350 1355 1360
 Asn Tyr Arg Thr Asp Leu Glu Gly Tyr Ala Val Asp Val His Gly Ile
 1365 1370 1375
 Glu Val His Lys Pro Leu Leu Leu Lys Glu Asp Met Asn Gly Thr Pro
 1380 1385 1390
 Gln Ala Thr Pro Phe Arg Ile Glu Val Arg Tyr Pro Ile Gln Ser Thr
 1395 1400 1405
 Thr Ala Leu Met Ser Ile Ser Thr Thr Gly Pro Asn Gly Gln His Ile
 1410 1415 1420
 Lys His Ala Asn Cys Glu Leu Arg Leu Glu His Pro Ser Gln Trp Glu
 425 1430 1435 1440
 Ala Glu Trp Asp Arg Gln Ala Tyr Leu Ile Asn Arg Ser Val Asn Cys
 1445 1450 1455
 Leu Leu Gln Arg Ser Ala Gln Gly Leu Asp Ser Met Leu Ala Thr Gly
 1460 1465 1470
 Met Val Tyr Lys Val Phe Ser Ser Leu Val Asp Tyr Ala Asp Gly Tyr
 1475 1480 1485
 Lys Gly Leu Gln Glu Val Val Leu His Ser Gln Glu Leu Glu Gly Thr
 1490 1495 1500
 Ala Lys Val Arg Phe Gln Thr Pro Ser Gly Gly Phe Val Cys Asn Pro
 505 1510 1515 1520
 Met Trp Ile Asp Ser Cys Gly Gln Thr Thr Gly Phe Met Met Asn Cys
 1525 1530 1535
 His Gln Thr Thr Pro Asn Asp Tyr Val Tyr Val Asn His Gly Trp Lys
 1540 1545 1550
 Ser Met Arg Leu Ala Lys Ala Phe Arg Glu Asp Gly Thr Tyr Arg Thr
 1555 1560 1565

25

Tyr Ile Arg Met Arg Pro Ile Asp Ser Thr Lys Phe Ala Gly Asp Leu
 1570 1575 1580
 Tyr Ile Leu Asp Glu Asp Asp Thr Val Val Gly Val Tyr Gly Asp Ile
 585 1590 1595 1600
 Thr Phe Gln Gly Leu Pro Arg Arg Val Leu Asn Thr Val Leu Pro Ser
 1605 1610 1615
 Ala Asn Ala Val Pro Val Asp Ala Pro Met Gly Arg Arg Asp Val Pro
 1620 1625 1630
 Pro Ser Arg Met Asp Val Pro Pro Val Arg Ser Gly Glu Gly Pro Pro
 1635 1640 1645
 Thr Ser Ala Pro Thr Gln Gln Ala Ile Ala Leu Pro Phe Ala Ala Asp
 1650 1655 1660
 Thr Ser Met Asp Ser Arg Leu Arg Pro Leu Leu Arg Ile Leu Ser Glu
 665 1670 1675 1680
 Glu Ile Gly Leu Gly Leu Asp Val Leu Ser Asp Asp Glu Leu Asp Phe
 1685 1690 1695
 Ala Asp His Gly Val Asp Ser Leu Leu Ser Leu Thr Ile Thr Gly Arg
 1700 1705 1710
 Met Arg Glu Glu Leu Gly Leu Asp Val Glu Ser Thr Ala Phe Met Asn
 1715 1720 1725
 Cys Pro Thr Leu Gly Ser Phe Lys Leu Phe Leu Gly Leu Val Asp Gln
 1730 1735 1740
 Asp Asn Lys Gly Ser Ser Gly Ser Asp Gly Ser Gly Arg Ser Ser Pro
 745 1750 1755 1760
 Ala Pro Gly Thr Glu Ser Gly Ala Thr Thr Pro Pro Met Ser Glu Glu
 1765 1770 1775
 Asp Gln Asp Lys Ile Val Ser Ser His Ser Leu His Gln Phe Gln Ala
 1780 1785 1790
 Ser Ser Thr Leu Leu Gln Gly Ser Pro Ser Lys Ala Arg Ser Thr Leu
 1795 1800 1805
 Phe Leu Leu Pro Asp Gly Ser Gly Ser Ala Thr Ser Tyr Ala Ser Leu
 1810 1815 1820
 Pro Pro Ile Ser Pro Asp Gly Asp Val Ala Val Tyr Gly Leu Asn Cys
 825 1830 1835 1840
 Pro Trp Leu Lys Asp Ser Ser Tyr Leu Val Glu Phe Gly Leu Lys Gly
 1845 1850 1855
 Leu Thr Glu Leu Tyr Val Asn Glu Ile Leu Arg Arg Lys Pro Gln Gly
 1860 1865 1870

26

Pro Tyr Asn Leu Gly Gly Trp Ser Ala Gly Gly Ile Cys Ala Tyr Glu
 1875 1880 1885

Ala Ala Leu Ile Leu Thr Arg Ala Gly His Gln Val Asp Arg Leu Ile
 1890 1895 1900

Leu Ile Asp Ser Pro Asn Pro Val Gly Leu Glu Lys Leu Pro Pro Arg
 905 1910 1915 1920

Leu Tyr Asp Phe Leu Asn Ser Gln Asn Val Phe Gly Ser Asp Asn Pro
 1925 1930 1935

His Ser Thr Ala Gly Thr Ser Val Lys Ala Pro Glu Trp Leu Leu Ala
 1940 1945 1950

His Phe Leu Ala Phe Ile Asp Ala Leu Asp Ala Tyr Val Ala Val Pro
 1955 1960 1965

Trp Asp Ser Gly Leu Val Gly Leu Ala Ser Pro Leu Pro Ala Pro Pro
 1970 1975 1980

Gln Thr Tyr Met Leu Trp Ala Glu Asp Gly Val Cys Lys Asp Ser Asp
 985 1990 1995 2000

Ser Ala Arg Pro Glu Tyr Arg Asp Asp Asp Pro Arg Glu Met Arg Trp
 2005 2010 2015

Leu Leu Glu Asn Arg Thr Asn Phe Gly Pro Asn Gly Trp Glu Ala Leu
 2020 2025 2030

Leu Gly Gly Lys Glu Gly Leu Phe Met Asp Arg Ile Ala Glu Ala Asn
 2035 2040 2045

His Phe Ser Met Leu Lys Arg Gly Arg Asn Ala Glu Tyr Val Ser Ala
 2050 2055 2060

Phe Leu Ala Arg Ala Leu Asp Asn
 065 2070

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<211> 228

<212> DNA

<213> Fusarium graminearum

<220>

<221> CDS

<222> (1)..(228)

<400> 7

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agt ggg cct agc gct agt gtt gat acg gct tgc tcc tcc agt ctc gtt 96
 Ser Gly Pro Ser Ala Ser Val Asp Thr Ala Cys Ser Ser Ser Leu Val
 20 25 30

27

ggc ttg cac ttg gct tgt aat tcc ctc tgg aga aat gat tgc gat aca 144
 Gly Leu His Leu Ala Cys Asn Ser Leu Trp Arg Asn Asp Cys Asp Thr
 35 40 45

gct att gcg ggc gga acc aat gtc atg act aac cct gac aac ttc gct 192
 Ala Ile Ala Gly Gly Thr Asn Val Met Thr Asn Pro Asp Asn Phe Ala
 50 55 60

ggt ttg gac cga ggc cac ttc cta tct aga acc ggt 228
 Gly Leu Asp Arg Gly His Phe Leu Ser Arg Thr Gly
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<211> 76

<212> PRT

<213> *Fusarium graminearum*

<400> 8

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 20 25 30

Gly Leu His Leu Ala Cys Asn Ser Leu Trp Arg Asn Asp Cys Asp Thr
 35 40 45

Ala Ile Ala Gly Gly Thr Asn Val Met Thr Asn Pro Asp Asn Phe Ala
 50 55 60

Gly Leu Asp Arg Gly His Phe Leu Ser Arg Thr Gly
 65 70 75

<210> 9

<211> 6534

<212> DNA

<213> *Wagiella dermatidis*

<400> 9

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 gtcagattcg aaaaccagaa ccgatcacat ccttccaaag cagtccctaa tttctctacc 180
 atccaagagc ttgtcgaccg ttattacaga ggtgacgcga aggatgccgc gaccgagagt 240
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 gtccggatag cgttcagagc tgggtgccac gtgggaaaag ttgcacagca gacagaatgt 480
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acaacgaagg	tcacgctgga	agaccactcc	acctggagta	cagtgccacc	gcagggaacg	1080
cgtcattcaa	aacgagaggc	tgatatcgct	attgtcggct	tctctggctg	cttccccgac	1140
gccgcagata	atgagctttt	ctggcaattg	ttggaacgtg	gcttggatgt	tcaccggccg	1200
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<211> 2177

<212> PRT

<213> Wagiella dermatidis

<400> 10

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      20             25             30

Phe Leu Glu Arg Ala Gly Glu Ala Val Arg Phe Glu Asn Gln Asn Arg
      35             40             45

Ser His Pro Ser Lys Ala Val Pro Asn Phe Ser Thr Ile Gln Glu Leu
      50             55             60

Val Asp Arg Tyr Tyr Arg Gly Asp Ala Lys Asp Ala Ala Thr Glu Ser
      65             70             75             80

Ala Leu Val Cys Ile Ser Gln Phe Cys His Phe Ile Gly Ala Phe Glu
      85             90             95

Glu Arg Arg Pro Ser Tyr Ile Gln Pro Asn Ser Asp Ala Arg Leu Val
      100            105            110

Gly Leu Cys Thr Gly Leu Ile Ala Ala Thr Ala Val Ala Ala Ser Asp
      115            120            125

Ser Leu Thr Ala Leu Ile Pro Leu Ala Val Glu Ala Val Arg Ile Ala
      130            135            140

Phe Arg Ala Gly Ala His Val Gly Lys Val Ala Gln Gln Thr Glu Cys
      145            150            155            160

Asp Ser Lys Thr Gln Ser Trp Ser Thr Ile Val Ala Ala Asp Glu Lys
      165            170            175

Ser Ala Gln Glu Ala Leu Asp Ala Phe His Lys Glu Xaa Gly Thr Ser
      180            185            190

Pro Ile Asn Gln Leu Trp Ile Ser Val Ser Ser Ala Thr Ser Val Thr
      195            200            205

Ile Ser Val Pro Pro Trp Thr Lys Ala Arg Leu Xaa Glu Glu Ser Glu
      210            215            220

Phe Phe Arg Thr Gln Lys Ser Ala Pro Val Ser Ile Phe Ala Pro Tyr
      225            230            235            240

His Ala Ser His Xaa His Ser Gln Ser Asp Leu Asp Lys Ile Leu Arg
      245            250            255

Pro Gln Thr Lys Thr Ile Phe Gly Asn Thr Thr Val Arg Phe Pro Val
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31

Cys	Ser	Ser	Val	Thr	Gly	Lys	Pro	Phe	Asn	Ala	Glu	Asn	Gly	Phe	Glu	275	280	285
Leu	Leu	Gln	Ala	Ala	Leu	Lys	Glu	Ile	Ile	Ile	Asp	Pro	Leu	Arg	Trp	290	295	300
Asp	Lys	Val	Leu	Lys	Tyr	Cys	Ala	Ala	Gly	Lys	Ala	Ser	Glu	Ala	Lys	305	310	315
Val	Phe	Ala	Val	Gly	Pro	Thr	Asn	Leu	Ala	Ser	Ser	Val	Val	Ser	Ala	325	330	335
Leu	Lys	Ala	Ser	Thr	Thr	Lys	Val	Thr	Leu	Glu	Asp	His	Ser	Thr	Trp	340	345	350
Ser	Thr	Val	Pro	Pro	Gln	Gly	Thr	Arg	His	Ser	Lys	Arg	Glu	Ala	Asp	355	360	365
Ile	Ala	Ile	Val	Gly	Phe	Ser	Gly	Arg	Phe	Pro	Asp	Ala	Ala	Asp	Asn	370	375	380
Glu	Leu	Phe	Trp	Gln	Leu	Leu	Glu	Arg	Gly	Leu	Asp	Val	His	Arg	Pro	385	390	395
Val	Pro	Pro	Asp	Arg	Phe	Pro	Val	Glu	Ser	His	Thr	Asp	Pro	Ser	Gly	405	410	415
Lys	Lys	Lys	Asn	Thr	Ser	His	Thr	Pro	Phe	Gly	Asn	Phe	Ile	Glu	Lys	420	425	430
Pro	Gly	Leu	Phe	Asp	Ala	Arg	Phe	Phe	Asn	Met	Ser	Pro	Arg	Glu	Ala	435	440	445
Ala	Gln	Thr	Asp	Pro	Met	Gln	Arg	Leu	Met	Leu	Thr	Thr	Gly	Tyr	Xaa	450	455	460
Ala	Met	Glu	Met	Ala	Gly	Ile	Val	Pro	Gly	Xaa	Thr	Pro	Ser	Thr	Xaa	465	470	475
His	Asp	Arg	Ile	Gly	Thr	Phe	Tyr	Gly	Gln	Thr	Ser	Xaa	Xaa	Trp	Arg	485	490	495
Glu	Val	Asn	Ala	Ala	Xaa	Asp	Ile	Asp	Thr	Tyr	Phe	Ile	Ser	Gly	Gly	500	505	510
Val	Arg	Ala	Phe	Gly	Pro	Gly	Xaa	Ile	Asn	Tyr	Phe	Phe	Lys	Phe	Ser	515	520	525
Gly	Pro	Xaa	Phe	Ser	Val	Asp	Met	Xaa	Ala	Asn	Pro	Ala	Trp	Pro	Xaa	530	535	540
Met	Asn	Val	Ala	Ile	Thr	Ser	Leu	Arg	Ala	Asn	Glu	Cys	Asp	Thr	Val	545	550	555
Phe	Thr	Gly	Gly	Ala	Asn	Val	Leu	Thr	Asn	Ser	Asp	Ile	Phe	Ser	Gly	565	570	575

32

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Ile	Met	Lys	Arg	Leu	Asp	Asp	Ala	Leu	Ala	Asp	Arg	Asp	Pro	Val	Leu
	610					615					620				
Gly	Val	Ile	Arg	Gly	Ile	Gly	Thr	Asn	His	Ser	Ala	Glu	Ala	Val	Ser
625					630					635					640
Ile	Thr	His	Pro	Cys	Ala	Glu	Asn	Gln	Ala	Phe	Leu	Phe	Asp	Lys	Val
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Leu	Lys	Glu	Cys	Asn	Val	His	Cys	Asn	Asp	Val	Asn	Tyr	Val	Glu	Met
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Ser	Ser	Val	Phe	Ala	Pro	Arg	Gln	Pro	Arg	Arg	Arg	Pro	Asp	Gln	Pro
	690					695					700				
Leu	Tyr	Val	Gly	Ala	Val	Lys	Ser	Asn	Ile	Gly	His	Gly	Glu	Ala	Val
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Ser	Gly	Val	Ser	Ala	Leu	Ile	Lys	Val	Leu	Leu	Met	Leu	Gln	Lys	Asn
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Lys	Ile	Pro	Pro	His	Thr	Gly	Ile	Lys	Lys	Gln	Ile	Asn	Lys	Asn	Phe
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Ala	Pro	Asp	Leu	Lys	Glu	Arg	Asn	Val	Asn	Ile	Ala	Phe	Gln	Thr	Thr
		755					760					765			
Pro	Phe	Pro	Arg	Pro	Pro	Gly	Gly	Lys	Arg	Thr	Val	Phe	Ile	Asn	Asn
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Phe	Ser	Ala	Ala	Gly	Gly	Asn	Thr	Ala	Met	Leu	Leu	Gln	Asp	Gly	Pro
785					790					795					800
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Ala	Tyr	Thr	Val	Thr	Ala	Arg	Arg	Ala	His	Tyr	Ser	Leu	Pro	Arg	Arg
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33

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 Met Ala Phe Thr Gly Gln Gly Ser Gln Tyr Thr Gly Met Gly Gln Lys
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 Gly Ser Val Glu Val Gln His Leu Pro Pro Thr Val Val Gln Leu Gly
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34

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 Tyr Leu Ser Thr Ser Val Gln Gly Ile Val Ser Glu Glu Val Lys Gly
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 1460 1465 1470
 Gln Asn Val Val Phe Asp Gly Pro Glu Phe Glu Ala Thr Ser Asn Ile
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35

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36

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 1985 1990 1995 2000
 Xaa Ile Thr Xaa Gln Leu Xaa Asp Leu Gln Xaa Leu His Pro Asp Lys
 2005 2010 2015
 Asn Tyr Thr Val Glu Lys Leu Asn Leu Ile Xaa Ser Pro Cys Pro Ile
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 Arg Leu Glu Pro Leu Pro Ala Arg Leu His His Phe Phe Asp Glu Ile
 2035 2040 2045
 Gly Leu Leu Gly Thr Gly Thr Gly Lys Thr Pro Asn Trp Leu Leu Pro
 2050 2055 2060
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 2065 2070 2075 2080
 Lys Ser Thr Arg Asp Phe Asn Ala Pro Pro Thr Leu Leu Ile Trp Ala
 2085 2090 2095

37

Thr Asp Gly Val Cys Gly Lys Pro Gly Asp Pro Arg Pro Pro Pro Gln
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Phe Gly Pro Asn Gly Trp Asp Lys Leu Leu Gly Ala Glu Val Cys Lys
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<213> *Aspergillus parasiticus*

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          35              40              45
Leu Gln Ser Met Asn Thr Val Asp His Lys Leu Ala Arg Thr Ala Asp
          50              55              60
Leu Arg Gln Met Val Gln Lys Tyr Val Asp Gly Lys Leu Thr Pro Ala
          65              70              75              80
Phe Arg Thr Ala Leu Val Cys Leu Cys Gln Leu Gly Cys Phe Ile Arg
          85              90              95

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40

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Val Leu Gly Phe Cys Met Gly Ser Leu Ala Ala Val Ala Val Ser Cys	115	120	125
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Ile Ala Phe Arg Leu Gly Leu Cys Ala Leu Glu Met Arg Asp Arg Val	145	150	155
Asp Gly Cys Ser Asp Asp Arg Gly Asp Pro Trp Ser Thr Ile Val Trp	165	170	175
Gly Leu Asp Pro Gln Gln Ala Arg Asp Gln Ile Glu Val Phe Cys Arg	180	185	190
Thr Thr Asn Val Pro Gln Thr Arg Arg Pro Trp Ile Ser Cys Ile Ser	195	200	205
Lys Asn Ala Ile Thr Leu Ser Gly Ser Pro Ser Thr Leu Arg Ala Phe	210	215	220
Cys Ala Met Pro Gln Met Ala Gln His Arg Thr Ala Pro Ile Pro Ile	225	230	235
Cys Leu Pro Ala His Asn Gly Ala Leu Phe Thr Gln Ala Asp Ile Thr	245	250	255
Thr Ile Leu Asp Thr Thr Pro Thr Thr Pro Trp Glu Gln Leu Pro Gly	260	265	270
Gln Ile Pro Tyr Ile Ser His Val Thr Gly Asn Val Val Gln Thr Ser	275	280	285
Asn Tyr Arg Asp Leu Ile Glu Val Ala Leu Ser Glu Thr Leu Leu Glu	290	295	300
Gln Val Arg Leu Asp Leu Val Glu Thr Gly Leu Pro Arg Leu Leu Gln	305	310	315
Ser Arg Gln Val Lys Ser Val Thr Ile Val Pro Phe Leu Thr Arg Met	325	330	335
Asn Glu Thr Met Ser Asn Ile Leu Pro Asp Ser Phe Ile Ser Thr Glu	340	345	350
Thr Arg Thr Asp Thr Gly Arg Ala Ile Pro Ala Ser Gly Arg Pro Gly	355	360	365
Ala Gly Lys Cys Lys Leu Ala Ile Val Ser Met Ser Gly Arg Phe Pro	370	375	380
Glu Ser Pro Thr Thr Glu Ser Phe Trp Asp Leu Leu Tyr Lys Gly Leu	385	390	395
			400

41

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Cys	Trp	Leu	Asp	Phe	Ser	Gly	Asp	Phe	Asp	Pro	Arg	Phe	Phe	Gly	Ile	435	440	445
Ser	Pro	Lys	Glu	Ala	Pro	Gln	Met	Asp	Pro	Ala	Gln	Arg	Met	Ala	Leu	450	455	460
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Thr	Pro	Ser	Thr	Gln	Arg	Asp	Arg	Ile	Gly	Val	Phe	His	Gly	Val	Thr	485	490	495
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Cys	Phe	Glu	Phe	Ala	Gly	Pro	Ser	Tyr	Thr	Asn	Asp	Thr	Ala	Cys	Ser	530	535	540
Ser	Ser	Leu	Ala	Ala	Ile	His	Leu	Ala	Cys	Asn	Ser	Leu	Trp	Arg	Gly	545	550	555
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Asp	Gly	His	Thr	Gly	Leu	Asp	Lys	Gly	Phe	Phe	Leu	Ser	Arg	Thr	Gly	580	585	590
Asn	Cys	Lys	Pro	Tyr	Asp	Asp	Lys	Ala	Asp	Gly	Tyr	Cys	Arg	Ala	Glu	595	600	605
Gly	Val	Gly	Thr	Val	Phe	Ile	Lys	Arg	Leu	Glu	Asp	Ala	Leu	Ala	Asp	610	615	620
Asn	Asp	Pro	Ile	Leu	Gly	Val	Ile	Leu	Asp	Ala	Lys	Thr	Asn	His	Ser	625	630	635
Ala	Met	Ser	Glu	Ser	Met	Thr	Arg	Pro	His	Val	Gly	Ala	Gln	Ile	Asp	645	650	655
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Ser	Tyr	Ile	Glu	Met	His	Gly	Thr	Gly	Thr	Gln	Val	Gly	Asp	Ala	Val	675	680	685
Glu	Met	Glu	Ser	Val	Leu	Ser	Val	Phe	Ala	Pro	Ser	Glu	Thr	Ala	Arg	690	695	700

42

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Phe	Leu	His	Val	Cys	Thr	Ser	Pro	Lys	Gly	Asp	Val	Glu	Glu	Met	Ala	
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Pro	Val	Val	Val	Gln	Leu	Ala	Ile	Thr	Cys	Leu	Gln	Met	Ala	Leu	Thr	
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Ser	Leu	Gly	Glu	Phe	Ala	Ala	Leu	Tyr	Ala	Ala	Gly	Val	Leu	Ser	Ala	
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43

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 Asp Pro Ser Lys Glu Ala Phe Pro Glu Ile Lys Thr Thr Thr Thr Leu
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44

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 Ser Tyr Gln Val Tyr Thr Lys Met Gly Gln Ala Lys Glu Asn Asp Leu
 1585 1590 1595 1600
 Val His Gly Asp Val Val Val Leu Asp Gly Glu Gln Ile Val Ala Phe
 1605 1610 1615

45

Phe Arg Gly Leu Thr Leu Arg Ser Val Pro Arg Gly Ala Leu Arg Val
 1620 1625 1630
 Val Leu Gln Thr Thr Val Lys Lys Ala Asp Arg Gln Leu Gly Phe Lys
 1635 1640 1645
 Thr Met Pro Ser Pro Pro Pro Pro Thr Thr Thr Met Pro Ile Ser Pro
 1650 1655 1660
 Tyr Lys Pro Ala Asn Thr Gln Val Ser Ser Gln Ala Ile Pro Ala Glu
 1665 1670 1675 1680
 Ala Thr His Ser His Thr Pro Pro Gln Pro Lys His Ser Pro Val Pro
 1685 1690 1695
 Glu Thr Ala Gly Ser Ala Pro Ala Ala Lys Gly Val Gly Val Ser Asn
 1700 1705 1710
 Glu Lys Leu Asp Ala Val Met Arg Val Val Ser Glu Glu Ser Gly Ile
 1715 1720 1725
 Ala Leu Glu Glu Leu Thr Asp Asp Ser Asn Phe Ala Asp Met Gly Ile
 1730 1735 1740
 Asp Ser Leu Ser Ser Met Val Ile Gly Ser Arg Phe Arg Glu Asp Leu
 1745 1750 1755 1760
 Gly Leu Asp Leu Gly Pro Glu Phe Ser Leu Phe Ile Asp Cys Thr Thr
 1765 1770 1775
 Val Arg Ala Leu Lys Asp Phe Met Leu Gly Ser Gly Asp Ala Gly Ser
 1780 1785 1790
 Gly Ser Asn Val Glu Asp Pro Pro Pro Ser Ala Thr Pro Gly Ile Asn
 1795 1800 1805
 Pro Glu Thr Asp Trp Ser Ser Ser Ala Ser Asp Ser Ile Phe Ala Ser
 1810 1815 1820
 Glu Asp His Gly His Ser Ser Glu Ser Gly Ala Asp Thr Gly Ser Pro
 1825 1830 1835 1840
 Pro Ala Leu Asp Leu Lys Pro Tyr Cys Arg Pro Ser Thr Ser Val Val
 1845 1850 1855
 Leu Gln Gly Leu Pro Met Val Ala Arg Lys Thr Leu Phe Met Leu Pro
 1860 1865 1870
 Asp Gly Gly Gly Ser Ala Phe Ser Tyr Ala Ser Leu Pro Arg Leu Lys
 1875 1880 1885
 Ser Asp Thr Ala Val Val Gly Leu Asn Cys Pro Tyr Ala Arg Asp Pro
 1890 1895 1900
 Glu Asn Met Asn Cys Thr His Gly Ala Met Ile Glu Ser Phe Cys Asn
 1905 1910 1915 1920

46

Glu Ile Arg Arg Arg Gln Pro Arg Gly Pro Tyr His Leu Gly Gly Trp
 1925 1930 1935
 Ser Ser Gly Gly Ala Phe Ala Tyr Val Val Ala Glu Ala Leu Val Asn
 1940 1945 1950
 Gln Gly Glu Glu Val His Ser Leu Ile Ile Ile Asp Ala Pro Ile Pro
 1955 1960 1965
 Gln Ala Met Glu Gln Leu Pro Arg Ala Phe Tyr Glu His Cys Asn Ser
 1970 1975 1980
 Ile Gly Leu Phe Ala Thr Gln Pro Gly Ala Ser Pro Asp Gly Ser Thr
 1985 1990 1995 2000
 Glu Pro Pro Ser Tyr Leu Ile Pro His Phe Thr Ala Val Val Asp Val
 2005 2010 2015
 Met Leu Asp Tyr Lys Leu Ala Pro Leu His Ala Arg Arg Met Pro Lys
 2020 2025 2030
 Val Gly Ile Val Trp Ala Ala Asp Thr Val Met Asp Glu Arg Asp Ala
 2035 2040 2045
 Pro Lys Met Lys Gly Met His Phe Met Ile Gln Lys Arg Thr Glu Phe
 2050 2055 2060
 Gly Pro Asp Gly Trp Asp Thr Ile Met Pro Gly Ala Ser Phe Asp Ile
 2065 2070 2075 2080
 Val Arg Ala Asp Gly Ala Asn His Phe Thr Leu Met Gln Lys Glu His
 2085 2090 2095
 Val Ser Ile Ile Ser Asp Leu Ile Asp Arg Val Met Ala
 2100 2105
 <210> 13
 <211> 1986
 <212> PRT
 <213> *Aspergillus nidulans*
 <400> 13
 Met Glu Asp Pro Tyr Arg Val Tyr Leu Phe Gly Asp Gln Thr Gly Asp
 1 5 10 15
 Phe Glu Val Gly Leu Arg Arg Leu Leu Gln Ala Lys Asn His Ser Leu
 20 25 30
 Leu Ser Ser Phe Leu Gln Arg Ser Tyr His Ala Val Arg Gln Glu Ile
 35 40 45
 Ser His Leu Pro Pro Ser Glu Arg Ser Thr Phe Pro Arg Phe Thr Ser
 50 55 60
 Ile Gly Asp Leu Leu Ala Arg His Cys Glu Ser Pro Gly Asn Pro Ala
 65 70 75 80

47

Ile Glu Ser Val Leu Thr Cys Ile Tyr Gln Leu Gly Cys Phe Ile Asn
 85 90 95
 Tyr Tyr Gly Asp Leu Gly His Thr Phe Pro Ser His Ser Gln Ser Gln
 100 105 110
 Leu Val Gly Leu Cys Thr Gly Leu Leu Ser Cys Ala Ala Val Ser Cys
 115 120 125
 Ala Ser Asn Ile Gly Glu Leu Leu Lys Pro Ala Val Glu Val Val Val
 130 135 140
 Val Ala Leu Arg Leu Gly Leu Cys Val Tyr Arg Val Arg Lys Leu Phe
 145 150 155 160
 Gly Gln Asp Gln Ala Ala Pro Leu Ser Trp Ser Ala Leu Val Ser Gly
 165 170 175
 Leu Ser Glu Ser Glu Gly Thr Ser Leu Ile Asp Lys Phe Thr Arg Arg
 180 185 190
 Asn Val Ile Pro Pro Ser Ser Arg Pro Tyr Ile Ser Ala Val Cys Ala
 195 200 205
 Asn Thr Leu Thr Ile Ser Gly Pro Pro Val Val Leu Asn Gln Phe Leu
 210 215 220
 Asp Thr Phe Ile Ser Gly Lys Asn Lys Ala Val Met Val Pro Ile His
 225 230 235 240
 Gly Pro Phe His Ala Ser His Leu Tyr Glu Lys Arg Asp Val Glu Trp
 245 250 255
 Ile Leu Lys Ser Cys Asn Val Glu Thr Ile Arg Asn His Lys Pro Arg
 260 265 270
 Ile Pro Val Leu Ser Ser Asn Thr Gly Glu Leu Ile Val Val Glu Asn
 275 280 285
 Met Glu Gly Phe Leu Lys Ile Ala Leu Glu Glu Ile Leu Leu Arg Gln
 290 295 300
 Met Ser Trp Asp Lys Val Thr Asp Ser Cys Ile Ser Ile Leu Lys Ser
 305 310 315 320
 Val Gly Asp Asn Lys Pro Lys Lys Leu Leu Pro Ile Ser Ser Thr Ala
 325 330 335
 Thr Gln Ser Leu Phe Asn Ser Leu Lys Lys Ser Asn Leu Val Asn Ile
 340 345 350
 Glu Val Asp Gly Gly Ile Ser Asp Phe Ala Ala Glu Thr Gln Leu Val
 355 360 365
 Asn Gln Thr Gly Arg Ala Glu Leu Ser Lys Ile Ala Ile Ile Gly Met
 370 375 380

48

Ser Gly Arg Phe Pro Glu Ala Asp Ser Pro Gln Asp Phe Trp Asn Leu
 385 390 395 400
 Leu Tyr Lys Gly Leu Asp Val His Arg Lys Val Pro Glu Asp Arg Trp
 405 410 415
 Asp Ala Asp Ala His Val Asp Leu Thr Gly Thr Ala Thr Asn Thr Ser
 420 425 430
 Lys Val Pro Tyr Gly Cys Trp Ile Arg Glu Pro Gly Leu Phe Asp Pro
 435 440 445
 Arg Phe Phe Asn Met Ser Pro Arg Glu Ala Leu Gln Ala Asp Pro Ala
 450 455 460
 Gln Arg Leu Ala Leu Leu Thr Ala Tyr Glu Ala Leu Glu Gly Ala Gly
 465 470 475 480
 Phe Val Pro Asp Ser Thr Pro Ser Thr Gln Arg Asp Arg Val Gly Ile
 485 490 495
 Phe Tyr Gly Met Thr Ser Asp Asp Tyr Arg Glu Val Asn Ser Gly Gln
 500 505 510
 Asp Ile Asp Thr Tyr Phe Ile Pro Gly Gly Asn Arg Ala Phe Thr Pro
 515 520 525
 Gly Arg Ile Asn Tyr Tyr Phe Lys Phe Ser Gly Pro Ser Val Ser Val
 530 535 540
 Asp Thr Ala Cys Ser Ser Ser Leu Ala Ala Ile His Leu Ala Cys Asn
 545 550 555 560
 Ser Ile Trp Arg Asn Asp Cys Asp Thr Ala Ile Thr Gly Gly Val Asn
 565 570 575
 Ile Leu Thr Asn Pro Asp Asn His Ala Gly Leu Asp Arg Gly His Phe
 580 585 590
 Leu Ser Arg Thr Gly Asn Cys Asn Thr Phe Asp Asp Gly Ala Asp Gly
 595 600 605
 Tyr Cys Arg Ala Asp Gly Val Gly Thr Val Val Leu Lys Arg Leu Glu
 610 615 620
 Asp Ala Leu Ala Asp Asn Asp Pro Ile Leu Gly Val Ile Asn Gly Ala
 625 630 635 640
 Tyr Thr Asn His Ser Ala Glu Ala Val Ser Ile Thr Arg Pro His Val
 645 650 655
 Gly Ala Gln Ala Phe Ile Phe Lys Lys Leu Leu Asn Glu Ala Asn Val
 660 665 670
 Asp Pro Lys Asn Ile Ser Tyr Ile Glu Met His Gly Thr Gly Thr Gln
 675 680 685

49

Ala Gly Asp Ala Val Glu Met Gln Ser Val Leu Asp Val Phe Ala Pro	690	695	700
Asp His Arg Arg Gly Pro Gly Gln Ser Leu His Leu Gly Ser Ala Lys	705	710	715 720
Ser Asn Ile Gly His Gly Glu Ser Ala Ser Gly Val Thr Ser Leu Val	725	730	735
Lys Val Leu Leu Met Met Lys Glu Asn Met Ile Pro Pro His Cys Gly	740	745	750
Ile Lys Thr Lys Ile Asn His Asn Phe Pro Thr Asp Leu Ala Gln Arg	755	760	765
Asn Val His Ile Ala Leu Gln Pro Thr Ala Trp Asn Arg Pro Ser Phe	770	775	780
Gly Lys Arg Gln Ile Phe Leu Asn Asn Phe Ser Ala Ala Gly Gly Asn	785	790	795 800
Thr Ala Leu Leu Leu Glu Asp Gly Pro Val Ser Asp Pro Glu Gly Glu	805	810	815
Asp Lys Arg Arg Thr His Val Ile Thr Leu Ser Ala Arg Ser Gln Thr	820	825	830
Ala Leu Gln Asn Asn Ile Asp Ala Leu Cys Gln Tyr Ile Ser Glu Gln	835	840	845
Glu Lys Thr Phe Gly Val Lys Asp Ser Asn Ala Leu Pro Ser Leu Ala	850	855	860
Tyr Thr Thr Thr Ala Arg Arg Ile His His Pro Phe Arg Val Thr Ala	865	870	875 880
Ile Gly Ser Ser Phe Gln Glu Met Arg Asp Ser Leu Ile Ala Ser Ser	885	890	895
Arg Lys Glu Phe Val Ala Val Pro Ala Lys Thr Pro Gly Ile Gly Phe	900	905	910
Leu Phe Thr Gly Gln Gly Ala Gln Tyr Ala Ala Met Gly Lys Gln Leu	915	920	925
Tyr Glu Asp Cys Ser His Phe Arg Ser Ala Ile Glu His Leu Asp Cys	930	935	940
Ile Ser Gln Gly Gln Asp Leu Pro Ser Ile Leu Pro Leu Val Asp Gly	945	950	955 960
Ser Leu Pro Leu Ser Glu Leu Ser Pro Val Val Val Gln Leu Gly Thr	965	970	975
Thr Cys Val Gln Met Ala Leu Ser Ser Phe Trp Ala Ser Leu Gly Ile	980	985	990

50

Thr Pro Ser Phe Val Leu Gly His Ser Leu Gly Asp Phe Ala Ala Met
 995 1000 1005
 Asn Ala Ala Gly Val Leu Ser Thr Ser Asp Thr Ile Tyr Ala Cys Gly
 1010 1015 1020
 Arg Arg Ala Gln Leu Leu Thr Glu Arg Cys Gln Pro Gly Thr His Ala
 1025 1030 1035 1040
 Met Leu Ala Ile Lys Ala Pro Leu Val Glu Val Lys Gln Leu Leu Asn
 1045 1050 1055
 Glu Lys Val His Asp Met Ala Cys Ile Asn Ser Pro Ser Glu Thr Val
 1060 1065 1070
 Ile Ser Gly Pro Lys Ser Ser Ile Asp Glu Leu Ser Arg Ala Cys Ser
 1075 1080 1085
 Glu Lys Gly Leu Lys Ser Thr Ile Leu Thr Val Pro Tyr Ala Phe His
 1090 1095 1100
 Ser Ala Gln Val Glu Pro Ile Leu Glu Asp Leu Glu Lys Ala Leu Gln
 1105 1110 1115 1120
 Gly Ile Thr Phe Asn Lys Pro Ser Val Pro Phe Val Ser Ala Leu Leu
 1125 1130 1135
 Gly Glu Val Ile Thr Glu Ala Gly Ser Asn Ile Leu Asn Ala Glu Tyr
 1140 1145 1150
 Leu Val Arg His Cys Arg Glu Thr Val Asn Phe Leu Ser Ala Phe Glu
 1155 1160 1165
 Ala Val Arg Asn Ala Lys Leu Gly Gly Asp Gln Thr Leu Trp Leu Glu
 1170 1175 1180
 Val Gly Pro His Thr Val Cys Ser Gly Met Val Lys Ala Thr Leu Gly
 1185 1190 1195 1200
 Pro Gln Thr Thr Thr Met Ala Ser Leu Arg Arg Asp Glu Asp Thr Trp
 1205 1210 1215
 Lys Val Leu Ser Asn Ser Leu Ser Ser Leu Tyr Leu Ala Gly Val Asp
 1220 1225 1230
 Ile Asn Trp Lys Gln Tyr His Gln Asp Phe Ser Ser Ser His Arg Val
 1235 1240 1245
 Leu Pro Leu Pro Thr Tyr Lys Trp Asp Leu Lys Asn Tyr Trp Ile Pro
 1250 1255 1260
 Tyr Arg Asn Asn Phe Cys Leu Thr Lys Gly Ser Ser Met Ser Ala Ala
 1265 1270 1275 1280
 Ser Ala Ser Leu Gln Pro Thr Phe Leu Thr Thr Ser Ala Gln Arg Val
 1285 1290 1295

51

Val Glu Ser Arg Asp Asp Gly Leu Thr Ala Thr Val Val Val His Asn
 1300 1305 1310
 Asp Ile Ala Asp Pro Asp Leu Asn Arg Val Ile Gln Gly His Lys Val
 1315 1320 1325
 Asn Gly Ala Ala Leu Cys Pro Ser Ser Leu Tyr Ala Asp Ser Ala Gln
 1330 1335 1340
 Thr Leu Ala Glu Tyr Leu Ile Glu Lys Tyr Lys Pro Glu Leu Lys Gly
 1345 1350 1355 1360
 Ser Gly Leu Asp Val Cys Asn Val Thr Val Pro Lys Pro Leu Ile Ala
 1365 1370 1375
 Lys Thr Gly Lys Glu Gln Phe Arg Ile Ser Ala Thr Ala Asn Trp Val
 1380 1385 1390
 Asp Lys His Val Ser Val Gln Val Phe Ser Val Thr Ala Glu Gly Lys
 1395 1400 1405
 Lys Leu Ile Asp His Ala His Cys Glu Val Lys Leu Phe Asp Cys Met
 1410 1415 1420
 Ala Ala Asp Leu Glu Trp Lys Arg Gly Ser Tyr Leu Val Lys Arg Ser
 1425 1430 1435 1440
 Ile Glu Leu Leu Glu Asn Ser Ala Val Lys Gly Asp Ala His Arg Leu
 1445 1450 1455
 Arg Arg Gly Met Val Tyr Lys Leu Phe Ser Ala Leu Val Asp Tyr Asp
 1460 1465 1470
 Glu Asn Tyr Gln Ser Ile Arg Glu Val Ile Leu Asp Ser Glu His His
 1475 1480 1485
 Glu Ala Thr Ala Leu Val Lys Phe Gln Ala Pro Gln Ala Asn Phe His
 1490 1495 1500
 Arg Asn Pro Tyr Trp Ile Asp Ser Phe Gly His Leu Ser Gly Phe Ile
 1505 1510 1515 1520
 Met Asn Ala Ser Asp Gly Thr Asp Ser Lys Ser Gln Val Phe Val Asn
 1525 1530 1535
 His Gly Trp Asp Ser Met Arg Cys Leu Lys Lys Phe Ser Ala Asp Val
 1540 1545 1550
 Thr Tyr Arg Thr Tyr Val Arg Met Gln Pro Trp Arg Asp Ser Ile Trp
 1555 1560 1565
 Ala Gly Asn Val Tyr Ile Phe Glu Gly Asp Asp Ile Ile Ala Val Phe
 1570 1575 1580
 Gly Gly Val Lys Phe Gln Ala Leu Ser Arg Lys Ile Leu Asp Ile Ala
 1585 1590 1595 1600

52

Leu Pro Pro Ala Gly Leu Ser Lys Ala Gln Thr Ser Pro Ile Gln Ser
 1605 1610 1615
 Ser Ala Pro Gln Lys Pro Ile Glu Thr Ala Lys Pro Thr Ser Arg Pro
 1620 1625 1630
 Ala Pro Pro Val Thr Met Lys Ser Phe Val Lys Lys Ser Ala Gly Pro
 1635 1640 1645
 Ser Val Val Val Arg Ala Leu Asn Ile Leu Ala Ser Glu Val Gly Leu
 1650 1655 1660
 Ser Glu Ser Asp Met Ser Asp Asp Leu Val Phe Ala Asp Tyr Gly Val
 1665 1670 1675 1680
 Asp Ser Leu Leu Ser Leu Thr Val Thr Gly Lys Tyr Arg Glu Glu Leu
 1685 1690 1695
 Asn Leu Asp Met Asp Ser Ser Val Phe Ile Glu His Pro Thr Val Gly
 1700 1705 1710
 Asp Phe Lys Arg Phe Val Thr Gln Leu Ser Pro Ser Val Ala Ser Asp
 1715 1720 1725
 Ser Ser Ser Thr Asp Arg Glu Ser Glu Tyr Ser Phe Asn Gly Asp Ser
 1730 1735 1740
 Cys Ser Gly Leu Ser Ser Pro Ala Ser Pro Gly Thr Val Ser Pro Pro
 1745 1750 1755 1760
 Asn Glu Lys Val Ile Gln Ile His Glu Asn Gly Thr Met Lys Glu Ile
 1765 1770 1775
 Arg Ala Ile Ile Ala Asp Glu Ile Gly Val Ser Ala Asp Glu Ile Lys
 1780 1785 1790
 Ser Asp Glu Asn Leu Asn Glu Leu Gly Met Asp Ser Leu Leu Ser Leu
 1795 1800 1805
 Thr Val Leu Gly Lys Ile Arg Glu Ser Leu Asp Met Asp Leu Pro Gly
 1810 1815 1820
 Glu Phe Phe Ile Glu Asn Gln Thr Leu Asp Gln Ile Glu Thr Ala Leu
 1825 1830 1835 1840
 Asp Leu Lys Pro Lys Ala Val Pro Thr Ala Val Pro Gln Ser Gln Pro
 1845 1850 1855
 Ile Thr Leu Pro Gln Ser Gln Ser Thr Lys Gln Leu Ser Thr Arg Pro
 1860 1865 1870
 Thr Ser Ser Ser Asp Asn His Pro Pro Ala Thr Ser Ile Leu Leu Gln
 1875 1880 1885
 Gly Asn Pro Arg Thr Ala Ser Lys Thr Leu Phe Leu Phe Pro Asp Gly
 1890 1895 1900

53

Ser Gly Ser Ala Thr Ser Tyr Ala Thr Ile Pro Gly Val Ser Pro Asn
1905 1910 1915 1920

Val Ala Val Tyr Gly Leu Asn Cys Pro Tyr Met Lys Ala Pro Glu Lys
1925 1930 1935

Leu Thr Cys Ser Leu Asp Ser Leu Thr Thr Pro Tyr Leu Ala Glu Ile
1940 1945 1950

Arg Arg Arg Gln Pro Thr Gly Pro Tyr Asn Leu Gly Gly Trp Ser Gln
1955 1960 1965

Ala Gly Ser Ala His Thr Thr Arg His Ala Ser Ser Tyr Cys Ser Arg
1970 1975 1980

Ala Lys
1985

<210> 14
<211> 53
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
atgaagcttg gggtttgagg gccaatggaa cgaaactagt gtaccacttg acc 53

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
gacagatctg ggcgcattcg ccattcag 28

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ggaatcggtc aatacactac 20

<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

tgtagatctc tattcctttg ccctcggacg agt

33

<210> 18

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 18

ggccgccacg gatattcttg ccaaagaatt cctgg

35

<210> 19

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 19

cggtgcctat agaaccggtt tcttaaggac cgcgc

35

<210> 20

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

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gayccmgtty ttyaayatg

19

<210> 21

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 21

gtccgtccrt gcatytc

17

<210> 22

<211> 34

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
ataagaatgc ggccgcaatg gccctcgaaa cagc 34

<210> 23
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
aatggcgcg ccgcccagc aatgacacc 29

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
tgccacctgt agtctgcaat cag 23

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
tgactaacc tgacaacttc gctg 24

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
ccaggatccg actgctcag 19

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 27

ctacatcgag atgcacggca c

21

<210> 28

<211> 16

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 28

ngtcgaswga nawgaa

16

<210> 29

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

gtncgaswca nawgtt

16

<210> 30

<211> 16

<212> DNA

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<220>

<223> Description of Artificial Sequence: Primer

<400> 30

wgtgnagwan canaga

16

<210> 31

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31

ntcgastwts gwggtt

15

<210> 32

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 32

tgwgnagwan casaga

16

<210> 33

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

agwgnagwan cawagg

16

<210> 34

<211> 14

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 34

cawcgcngaa sgaa

14

<210> 35

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 35

tcstcgnact wgga

14

<210> 36

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 36

ttgttactgg agaggtaatg aag

23

<210> 37

<211> 23

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
tgagacagat ctgcgagacc etc 23

<210> 38
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
atgtctccaa aggaagctga gc 22

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
tcgagtgatg gatactgctt cg 22

<210> 40
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 40
cggctacact agaaggacag tatttggtta 29

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 41
gtcaggcaac tatggatgaa cgaaatagac 30

<210> 42
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 42

acccatctca taaataacgt catgc 25

<210> 43

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 43

caactctatc agagcttggt tga 23

<210> 44

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 44

cccgattca tgagctttgt tcaaataagg 30

<210> 45

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 45

ttattctaga ttttccatgg gaatggatac agtcttacg 39

<210> 46

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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cgccaccatg gtgagcaagg gcgaggagct gtt 33

<210> 47

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 47

tatgatctag agtcgcgggc gctttacttg tacagctcg

39

<210> 48

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 48

gcttctaatac cgtactagtg gatca

25

<210> 49

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 49

ctttgatctt ttctacgggg tctga

25